UNITED STATES DEPARTMENT OF COMMERCE
Patent and Trademark Office
ASSISTANT SECRETARY AND COMMISSIONER
OF PATENTS AND TRADEMARKS
Washington, D.C. 20231

September 9, 2002

YANKWICH & ASSOCIATES
130 BISHOP ALLEN DRIVE
CAMBRIDGE, MA 02139
US

Dear Sir/Madam,

This is to deny your refund request in the amount of $3,928.00, for serial number 10/034,974.

In response to your request for reconsideration filed June 21, 2002 to the denial decision mailed June 10, 2002 is acknowledged.

A further review of the application record reveals there are clearly multiple dependent claims present in this application. Total claims including multiple dependent claims are 275 of which 2 is independent.

Enclosed is your copy of exhibit C. The Office made correction on the form to determine multiple dependent claims verses what Applicants' claim as independent claims.

Sincerely,

MARGARET STEVENS
Technical Center 1600
Refund Section, Office of Finance

Exhibit C

Designation of Claims and Fee Calculation
Applicants' Calculation vs. Office's Proposed Calculation
Ser. No. 10/034,974 (Wescott et al.)

Applicants' Designation	Fee	Claim Number	Office's Designation	Fee
Independent	0	1	Independent	0
Dependent	0	2	Dependent	0
Dependent	0	3	Dependent	0
Dependent	0	4	Dependent	0
Independent	0	5	Independent	0
Dependent	0	6	Dependent	0
Dependent	0	7	Dependent	0
Dependent	0	8	Dependent	0
Dependent	0	9	Dependent	0
Dependent	0	10	Dependent	0
Dependent	0	11	Dependent	0
Independent ND	0	12	Mult. Dependent (11)	36
Dependent	0	13	Mult. Dependent (11)	198
Dependent	0	14	Mult. Dependent (11)	198
Dependent	0	15	Mult. Dependent (11)	198
Independent ND	84	16	Mult. Dependent (11)	198
Dependent	0	17	Mult. Dependent (11)	198
Dependent	0	18	Mult. Dependent (11)	198
Independent ND	84	19	Mult. Dependent (11)	198
Independent ND	84	20	Mult. Dependent (11)	198
Dependent	18	21	Mult. Dependent (11)	198
Dependent	18	22	Mult. Dependent (11)	198
Dependent	18	23	Mult. Dependent (11)	198
Dependent	18	24	Mult. Dependent (11)	198
Independent ND	102	25	Mult. Dependent (11)	198
Independent ND	102	26	Mult. Dependent (11)	198
Independent ND	102	27	Mult. Dependent (11)	198
Dependent	18	28	Mult. Dependent (11)	198
Dependent	18	29	Mult. Dependent (11)	198
Dependent	18	30	Mult. Dependent (11)	198
Dependent	18	31	Mult. Dependent (11)	198
Independent ND	102	32	Mult. Dependent (11)	198
Dependent	18	33	Mult. Dependent (11)	198
Dependent	18	34	Mult. Dependent (11)	198
Independent ND	102	35	Mult. Dependent (11)	198
Basic Filing Fee	740	—	**Basic Filing Fee**	740
Mult. Dependent fee	0	—	**Mult. Dependent fee**	280
Total Fees	**1682**	—	**Total Fees**	**5610**

CLAIMS OF U.S. SER. NO. 10/034,974 AS ORIGINALLY FILED

(Independent claims in **BOLD** type)

independent

1. **An isolated polypeptide having the ability to bind to fibrin comprising the amino acid sequence: Cys–X_2–X_3–X_4–X_5–X_6–X_7–X_8–Cys (SEQ ID NO: 2), wherein**
X_2 is Pro, Arg, Asn, Asp, Gln, Gly, Phe, Ser, Thr or Tyr;
X_3 is Ala, Asn, Asp, Gln, Glu, Gly, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val;
X_4 is Glu, Gly, Lys, Ser, or Tyr;
X_5 is Pro, Asp, Glu, Asn, Gln, Glu, Gly, Leu, Lys, Ser, Thr, or Tyr;
X_6 is Arg, Gly, or Trp;
X_7 is Leu, Ile, Lys, Met, Asn, Gln, Pro, Ser, Thr, or Val; and
X_8 is Ile, Leu, Phe, Trp, or Tyr.

2. The polypeptide according to Claim 1, comprising the amino acid sequence: Cys–X_2–X_3–X_4–X_5–Trp–X_7–X_8–Cys (SEQ ID NO: 42), wherein
X_2 is Pro, Asn, Gln, Ser, or Thr;
X_3 is Ala, Asn, Asp, Gln, Glu, Gly, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val;
X_4 is Glu or Ser;
X_5 is Pro, Asp, Glu, Asn, Gln, Ser, Thr, or Tyr;
X_7 is Leu, Ile, Met, Asn, Gln, Ser, Thr, or Val; and
X_8 is Phe, Trp, or Tyr.

3. The polypeptide according to Claim 1, wherein the following amino acid positions are independently selected as follows: the amino acid residue X_2 is Pro, the amino acid residue X_3 is Asp, Glu, Gly, Met, or Trp, the amino acid residue X_4 is Glu, the amino acid residue X_5 is Asn, Asp, Glu, Pro, or Ser, the amino acid residue X_6 is Trp, the amino acid residue X_7 is Leu or Thr, the amino acid residue X_8 is Phe, or combinations of such selections.

4. The polypeptide according to Claim 1, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of:
Cys-Ser-Asp-Glu-Asn-Trp-Leu-Trp-Cys (SEQ ID NO: 21),
Cys-Pro-Met-Ser-Glu-Trp-Leu-Tyr-Cys (SEQ ID NO: 22),
Cys-Pro-Trp-Glu-Ser-Trp-Thr-Phe-Cys (SEQ ID NO: 23),
Cys-Gln-Glu-Glu-Pro-Trp-Leu-Phe-Cys (SEQ ID NO: 24),
Cys-Pro-Gly-Glu-Asp-Trp-Leu-Phe-Cys (SEQ ID NO: 25),
Cys-Tyr-Gly-Glu-Ser-Gly-Ile-Phe-Cys (SEQ ID NO:43);
Cys-Thr-Gly-Glu-Pro-Gly-Pro-Ile-Cys (SEQ ID NO:44);
Cys-Gln-Leu-Gly-Tyr-Arg-Thr-Tyr-Cys (SEQ ID NO:45);
Cys-Asp-Gly-Glu-Pro-Trp-Leu-Phe-Cys (SEQ ID NO:46);
Cys-Gly-Trp-Gly-Ser-Trp-Lys-Phe-Cys (SEQ ID NO:47);
Cys-Gly-Trp-Gly-Ser-Gly-Lys-Leu-Cys (SEQ ID NO:48);
Cys-Pro-Gly-Glu-Pro-Trp-Thr-Phe-Cys (SEQ ID NO:49);
Cys-Pro-Gly-Glu-Pro-Trp-Thr-Phe-Cys (SEQ ID NO:50);
Cys-Pro-Gly-Tyr-Leu-Arg-Ser-Leu-Cys (SEQ ID NO:51);
Cys-Pro-Gly-Glu-Pro-Trp-Ser-Phe-Cys (SEQ ID NO:52);
Cys-Arg-Gly-Glu-Ser-Trp-Pro-Tyr-Cys (SEQ ID NO:53);
Cys-Pro-Gly-Tyr-Lys-Arg-Gln-Phe-Cys (SEQ ID NO:54);
Cys-Gly-Gln-Glu-Ser-Arg-Thr-Phe-Cys (SEQ ID NO:55); and
Cys-Phe-Gln-Lys-Gly-Gly-Thr-Leu-Cys (SEQ ID NO:56).

independent

5. **A fibrin binding polypeptide comprising the amino acid sequence: Cys-Asp-Tyr-Tyr-Gly-Thr-Cys (SEQ ID NO: 26).**

6. The polypeptide according to Claim 1, comprising the amino acid sequence:
X_1–X_2–X_3–X_4–X_5–X_6–X_7–X_8–X_9–X_{10}–X_{11}–X_{12}–X_{13}–X_{14}–X_{15} (SEQ ID NO:1),
wherein
X_1 is Cys, Pro, or Trp;
X_2 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val, or if X_4 and X_{12} are not Cys, then X_2 may be Cys;

X_3 is Ala, Asn, Gln, Gly, Ile, Leu, Met, Phe, Pro, or Thr;

X_4 is Cys or another amino acid capable of forming a covalent cross-link to X_{12};

X_5 is Pro, Arg, Asn, Asp, Gln, Gly, Phe, Ser, Thr or Tyr;

X_6 is Ala, Asn, Asp, Gln, Glu, Gly, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val;

X_7 is Glu, Gly, Lys, Ser, or Tyr;

X_8 is Pro, Asp, Glu, Asn, Gln, Glu, Gly, Leu, Lys, Ser, Thr, or Tyr;

X_9 is Arg, Gly, or Trp;

X_{10} is Leu, Ile, Lys, Met, Asn, Gln, Pro, Ser, Thr, or Val;

X_{11} is Ile, Leu, Phe, Trp, or Tyr;

X_{12} is Cys or another amino acid capable of forming a covalent cross-link to X_4;

X_{13} is Cys, Gly, Leu, Phe, Pro, Trp, or Tyr;

X_{14} is Pro, Ala, Gly, Asn, Gln, Lys, Ser, Thr, Tyr, Asp, Glu, or His; and

X_{15} is Ala, Arg, Asp, Ile, Leu, Met, Phe, Pro, Trp, Val, Asn, Gln, Gly, Ser, Thr, Tyr, or His.

7. The polypeptide according to Claim 6, comprising the amino acid sequence: Trp–X_2–X_3–X_4–X_5–X_6–X_7–X_8–Trp–X_{10}–X_{11}–X_{12}–X_{13}–X_{14}–X_{15} (SEQ ID NO:41), wherein

X_2 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val, or if X_4 and X_{12} are not Cys, then X_2 may be Cys;

X_3 is Ala, Asn, Gln, Gly, Ile, Leu, Met, Phe, or Pro;

X_4 is Cys or another amino acid capable of forming a covalent cross-link to X_{12};

X_5 is Pro, Asn, Gln, Ser, or Thr;

X_6 is Ala, Asn, Asp, Gln, Glu, Gly, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val;

X_7 is Glu or Ser;

X_8 is Pro, Asp, Glu, Asn, Gln, Ser, Thr, or Tyr;

X_{10} is Leu, Ile, Met, Asn, Gln, Ser, Thr, or Val;

X_{11} is Phe, Trp, or Tyr;

X_{12} is Cys or another amino acid capable of forming a covalent cross-link to X_4;

X_{13} is Phe, Trp, or Tyr;

X_{14} is Pro, Ala, Gly, Asn, Gln, Ser, Thr, Tyr, Asp, Glu, or His; and

X_{15} is Ala, Ile, Leu, Met, Phe, Pro, Trp, Val, Asn, Gln, Gly, Ser, Thr, Tyr, or His.

8. The polypeptide according to Claim 7, wherein the following amino acid positions are independently selected as follows: the amino acid residue X_2 is Ala, Gln, Glu, Lys, or Met; the amino acid residue X_3 is Ala, Leu, Met, or Pro; the amino acid residue X_4 is Cys; the amino acid residue X_5 is Pro; the amino acid residue X_6 is Asp, Glu, Gly, Met, or Trp; the amino acid residue X_7 is Glu; the amino acid residue X_8 is Asn, Asp, Glu, Pro, or Ser; the amino acid residue X_{10} is Leu or Thr; the amino acid residue X_{11} is Phe; the amino acid residue X_{12} is Cys; the amino acid residue X_{13} is Trp; the amino acid residue X_{14} is Asp, Gly, His, Phe, or Ser; the amino acid residue X_{15} is Ala, Gly, His, Pro, or Ser, or combinations of such selections.

9. The polypeptide according to Claim 8, wherein the following amino acid positions are independently selected as follows: the amino acid residue X_5 is Pro, the amino acid residue X_7 is Glu, the amino acid residue X_{10} is Leu, the amino acid residue X_{11} is Phe, the amino acid residue X_{13} is Trp, or combinations of such selections.

10. The polypeptide according to Claim 6, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of:
Trp-Glu-Leu-Cys-Ser-Asp-Glu-Asn-Trp-Leu-Trp-Cys-Trp-Pro-His (SEQ ID NO: 3),
Trp-Met-Met-Cys-Pro-Met-Ser-Glu-Trp-Leu-Tyr-Cys-Trp-Ser-Ala (SEQ ID NO: 4),
Trp-Gln-Pro-Cys-Pro-Trp-Glu-Ser-Trp-Thr-Phe-Cys-Trp-Asp-Pro (SEQ ID NO: 5),
Trp-Ala-Pro-Cys-Gln-Glu-Glu-Pro-Trp-Leu-Phe-Cys-Phe-His-Gly (SEQ ID NO: 6),
Trp-Lys-Ala-Cys-Pro-Gly-Glu-Asp-Trp-Leu-Phe-Cys-Trp-Gly-Ser (SEQ ID NO: 7),
Pro-Arg-Pro-Cys-Tyr-Gly-Glu-Ser-Gly-Ile-Phe-Cys-Trp-Lys-Val (SEQ ID NO:27);
Pro-Arg-Pro-Cys-Thr-Gly-Glu-Pro-Gly-Pro-Ile-Cys-Gly-Pro-Arg (SEQ ID NO:28);
Trp-Gln-Ala-Cys-Gln-Leu-Gly-Tyr-Arg-Thr-Tyr-Cys-Trp-Asp-Gly (SEQ ID NO:29);
Trp-Lys-Phe-Cys-Asp-Gly-Glu-Pro-Trp-Leu-Phe-Cys-Trp-Asp-Gly (SEQ ID NO:30);
Trp-Asn-Gly-Cys-Gly-Trp-Gly-Ser-Trp-Lys-Phe-Cys-Gly-Glu-Gly (SEQ ID NO:31);

Trp-Leu-Asn-Cys-Gly-Trp-Gly-Ser-Gly-Lys-Leu-Cys-Leu-Gly-Val (SEQ ID NO:32);

Cys-Tyr-Phe-Cys-Pro-Gly-Glu-Pro-Trp-Thr-Phe-Cys-Cys-Asp-Asp (SEQ ID NO:33);

Trp-His-Phe-Cys-Pro-Gly-Glu-Pro-Trp-Thr-Phe-Cys-Trp-Ala-Gly (SEQ ID NO:34);

Trp-Gln-Thr-Cys-Pro-Gly-Tyr-Leu-Arg-Ser-Leu-Cys-Trp-Asp-Gly (SEQ ID NO:35);

Trp-Tyr-Phe-Cys-Pro-Gly-Glu-Pro-Trp-Ser-Phe-Cys-Pro-Asp-Gly (SEQ ID NO:36);

Pro-Arg-Pro-Cys-Arg-Gly-Glu-Ser-Trp-Pro-Tyr-Cys-Trp-Gly-Gly (SEQ ID NO:37);

Trp-Gln-Ala-Cys-Pro-Gly-Tyr-Lys-Arg-Gln-Phe-Cys-Trp-Asp-Arg (SEQ ID NO:38);

Pro-Arg-Pro-Cys-Gly-Gln-Glu-Ser-Arg-Thr-Phe-Cys-Leu-Glu-Gly (SEQ ID NO:39); and

Pro-Arg-Pro-Cys-Phe-Gln-Lys-Gly-Gly-Thr-Leu-Cys-Trp-Pro-Gly (SEQ ID NO:40).

11. The polypeptide according to Claim 5, having the amino acid sequence: Arg-Ala-Pro-Cys-Asp-Tyr-Tyr-Gly-Thr-Cys-Val-Glu-Leu (SEQ ID NO: 8).

not independent

12. **A method of detecting fibrin in a mammalian subject comprising the steps of:**
    (a) detectably labeling a polypeptide according to any one of Claims 1–11;
    (b) administering to said subject the labeled polypeptide and, thereafter,
    (c) detecting the labeled polypeptide in the subject.

13. The method according to Claim 12, wherein said label is fluorescent, echogenic, radioactive or paramagnetic.

14. The method according to Claim 12, wherein said label is ^{111}In or ^{99m}Tc.

15. The method of according to Claim 12, wherein said detecting step is indicative of deep-vein thrombosis, pulmonary embolism, cardiogenic thrombosis, atherosclerosis or stroke.

not independent

16. A method of treating a disease inv lving thrombus formation, comprising the step:
administering to a mammalian subject in need of treatment for such a disease a composition comprising a polypeptide according to any one of Claims 1–11 conjugated with a pharmaceutical effective for treating said disease involving thrombus formation.

17. The method according to Claim 16, wherein said disease is deep-vein thrombosis, pulmonary embolism, cardiogenic thrombosis, atherosclerosis, myocardial infarct, reperfusion ischemia, or stroke.

18. The method according to Claim 16, wherein said pharmaceutical is a thrombolytic agent selected from tPA, streptokinase, and urokinase.

not independent

19. A recombinant host cell or bacteriophage expressing on its surface an exogenous fibrin binding polypeptide according to any one of Claims 1-11.

20. A magnetic resonance imaging contrast agent comprising at least one paramagnetic metal atom linked to at least one polypeptide according to any one of Claims 1–11.

21. The magnetic resonance imaging contrast agent according to Claim 20, wherein said magnetic resonance imaging contrast agent further comprises at least one chelator selected from the group consisting of DTPA, DOTA, EDTA, TETA, EHPG, HBED, NOTA, DOTMA, TETMA, PDTA, TTHA, LICAM, and MECAM.

22. The magnetic resonance imaging contrast agent according to Claim 21, wherein said chelator comprises diethylenetriamine or tetraazacyclododecane or a carboxymethyl-substituted derivative thereof.

23. The magnetic resonance imaging contrast agent according to Claim 21, wherein said paramagnetic metal atom is selected from the group consisting of: Mn^{2+}, Cu^{2+}, Fe^{2+}, Co^{2+}, Ni^{2+}, Gd^{3+}, Eu^{3+}, Dy^{3+}, Pr^{3+}, Cr^{3+}, Co^{3+}, Fe^{3+}, Ti^{3+}, Tb^{3+}, Nd^{3+}, Sm^{3+}, Ho^{3+}, Er^{3+}, Pa^{4+}, and Eu^{2+}.

24. The magnetic resonance imaging contrast agent according to Claim 23, wherein said paramagnetic metal atom is Gd^{3+}.

25. A method for identifying fibrin binding compounds comprising the steps of utilizing a fibrin binding polypeptide according to any one of Claims 1–11 to form a complex with a fibrin target, contacting said complex with one or more potential fibrin binding compounds, and determining whether said one or more potential fibrin binding compounds competes with said fibrin binding polypeptide to form a complex with said fibrin target.

26. A method for identifying fibrin binding compounds comprising the steps of contacting a solution containing a potential fibrin binding compound with fibrin target to form a complex between said compound and the fibrin target, contacting said complex with a fibrin binding polypeptide according to any one of Claims 1–11, and determining whether said fibrin binding polypeptide competes with said potential fibrin binding compound to form a complex with said fibrin target.

27. A diagnostic imaging agent comprising a polypeptide according to any one of Claims 1–11 linked to a detectable label.

28. The imaging agent according to Claim 27, wherein said polypeptide is radiolabeled.

29. The imaging agent according to Claim 27, wherein said polypeptide is labeled with ^{99m}Tc.

30. The imaging agent according to Claim 27, wherein said polypeptide is fluoresceinated.

31. The imaging agent according to Claim 27, wherein said polypeptide is linked to an echogenic label suitable for ultrasound imaging.

not independent

32. A method of medical imaging comprising the steps of administering to a mammalian subject a pharmaceutical preparation of a contrast agent comprising at least one polypeptide according to any one of Claims 1–11 and imaging said contrast agent by a step selected from the group consisting of magnetic resonance imaging, ultrasound imaging, optical imaging, sonoluminescence imaging, photoacoustic imaging, and nuclear imaging.

33. The method of medical imaging according to Claim 32, wherein said administering step is selected from among the group consisting of:
inhaling, transdermal absorbing, intramuscular injecting, subcutaneous injecting, intravenous injecting, and intra–arterial injecting.

34. The method of medical imaging according to Claim 32, wherein said pharmaceutical preparation is packaged in a container selected from among the group consisting of: kit, syringe, vial, bottle, flexible container, packet, or inhaler.

not independent

35. A method of purifying fibrin or fibrin-like polypeptide from a solution containing it comprising contacting the solution with at least one polypeptide according to any one of Claims 1–11, and then separating said polypeptide from said solution.

UNITED STATES DEPARTMENT OF COMMERCE
Patent and Trademark Office
ASSISTANT SECRETARY AND COMMISSIONER
OF PATENTS AND TRADEMARKS
Washington, D.C. 20231

June 10, 2002

YANKWICH & ASSOCIATES
130 BISHOP ALLEN DRIVE
CAMBRIDGE, MA 02139
US

Dear Sir/Madam,

This is to Deny your refund request in the amount of $2,532.00, for serial number 10/034974.

A review of the application record reveals that the application is under the multiple dependent program. In calculating the fees to include all claims that are multiple, total claims are 275 of which 2 claims are independent. The fee owed for 255 claims in excess of 20 is $4,590.00. The fee owed to participate under the multiple dependent program is $280.00

Sincerely,

MARGARET STEVENS
Technical Center 1600
Refund Section, Office of Finance

B

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of:	Wescott, et al.
Serial No.:	10/034,974
Filing Date:	December 21, 2001
Entitled:	FIBRIN BINDING MOIETIES USEFUL AS IMAGING AGENTS

Group Art Unit: 1645

Examiner: (not yet assigned)

Attorney Docket No. DYX-024.1 US

Commissioner for Patents
OFFICE OF FINANCE
Accounting Division- Refund Section
Washington, D.C. 20231

REQUEST FOR RECONSIDERATION OF DECISION TO DENY REFUND OF OVERPAID FEE

To the Office of Finance:

The undersigned attorney of record hereby requests reconsideration of a decision dated June 10, 2002, denying Applicants' request for a refund of overpaid filing fees made pursuant to the provisions of 37 CFR §1.26 in the above-identified patent application.

REMARKS

Applicants' attorney is in receipt of a decision, attached as Exhibit A, in which Applicants' previous request for a refund of excess filing fees charged against the deposit account of the undersigned attorney was denied.

The reason for this request for reconsideration is that the decision of June 10, 2002 (Exhibit A) does not provide an explanation of how the Office is distinguishing between independent and multiple dependent claims. The decision also refers to "the multiple dependent program", and Applicants request to know what this refers to and whether under this program the requirements of 37 CFR §1.75 and MPEP 608.01(n) have been suspended or superseded. Applicants also request to know whether "the multiple dependent program" has been published and request a citation for that publication.

Attached as Exhibit B is the pending claim set of the above-identified application, with independent claims indicated in **bold type**. Attached as Exhibit C is a table showing how Applicants have calculated their filing fees.

The decision of June 10, 2002 (Exhibit A) indicates that the Office regards the claim set (Exhibit B) as having 275 total claims and 2 independent claims. The total of fees based on this calculation is $5610.00, of which the totality has been paid by Applicants as follows: $1682.00 supplied by check at filing + $3928.00 charged against the undersigned attorney's deposit account on February 8, 2002.

The table in Exhibit C includes a column in which Applicants guess at the calculation of fees performed by the Office of Finance in making its decision of June 10, 2002. Confirmation that the table in Exhibit C reflects the Office's reasoning in this regard is requested. It is important for Applicants to understand the method of calculation used by the Office, because it appears to afford a means for converting independent claims to dependent claims, at least for fee calculation purposes.

If, upon reconsideration, the Applicants' method of calculation is deemed to be correct, Applicants hereby renew their request for a refund of $3928.00, representing the overcharge.

Respectfully submitted,

Leon R. Yankwich, Reg. No. 30,237
Attorney of Record
YANKWICH & ASSOCIATES
130 Bishop Allen Drive
Cambridge, Mass. 02139
tel. (617) 491-4343

CERTIFICATE OF MAILING BY FIRST CLASS MAIL

The undersigned hereby certifies that the this paper is being deposited with the U.S. Postal Service as First Class Mail, under 37 C.F.R. §1.8, postage prepaid, in an envelope addressed to the Commissioner for Patents, OFFICE OF FINANCE Accounting Division - Refund Section, Washington, D.C. 20231, on the date indicated below:

June 21, 2002
date of mailing and signature

Stephanie L. Leicht
Stephanie L. Leicht